

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- AY
- (i) APPLICANT: Lutticken, Heinrich D.
Mundt, Egbert
Loon, Adriaan A. W. M.
- (ii) TITLE OF INVENTION: Recombinant birnavirus vaccine
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Akzo Nobel Patent Dept.
(B) STREET: 1300 Piccard Drive, Suite 206
(C) CITY: Rockville
(D) STATE: Maryland
(E) COUNTRY: US
(F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30(EPO)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 26-MAY-1998
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Gormley, Mary E.
(B) REGISTRATION NUMBER: 34,409
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 301-948-7400
(B) TELEFAX: 301-948-9751

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2827 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:112..2745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGATACGATG GGTCTGACCC TCTGGGAGTC ACGAATTAAC GTGGCTACTA GGGGCGATAC 60
 CCGCCGCTGG CCGCCACGTT AGTGGCTCCT CTTCTTGATG ATTCTGCCAC C ATG AGT 117
 Met Ser
 1
 GAC ATT TTC AAC AGT CCA CAG GCG CGA AGC ACG ATC TCA GCA GCG TTC 165
 Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala Ala Phe
 5 10 15
 GGC ATA AAG CCT ACT GCT GGA CAA GAC GTG GAA GAA CTC TTG ATC CCT 213
 Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu Ile Pro
 20 25 30
 AAA GTT TGG GTG CCA CCT GAG GAT CCG CTT GCC AGC CCT AGT CGA CTG 261
 Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser Arg Leu
 35 40 45 50
 GCA AAG TTC CTC AGA GAG AAC GGC TAC AAA GTT TTG CAG CCA CGG TCT 309
 Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro Arg Ser
 55 60 65
 CTG CCC GAG AAT GAG GAG TAT GAG ACC GAC CAA ATA CTC CCA GAC TTA 357
 Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro Asp Leu
 70 75 80
 GCA TGG ATG CGA CAG ATA GAA GGG GCT GTT TTA AAA CCC ACT CTA TCT 405
 Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr Leu Ser
 85 90 95
 CTC CCT ATT GGA GAT CAG GAG TAC TTC CCA AAG TAC TAC CCA ACA CAT 453
 Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro Thr His
 100 105 110
 CGC CCT AGC AAG GAG AAG CCC AAT GCG TAC CCG CCA GAC ATC GCA CTA 501
 Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile Ala Leu
 115 120 125 130
 CTC AAG CAG ATG ATT TAC CTG TTT CTC CAG GTT CCA GAG GCC AAC GAG 549
 Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala Asn Glu
 135 140 145

GGC	CTA	AAG	GAT	GAA	GTA	ACC	CTC	TTG	ACC	CAA	AAC	ATA	AGG	GAC	AAG	597
Gly	Leu	Lys	Asp	Glu	Val	Thr	Leu	Leu	Thr	Gln	Asn	Ile	Arg	Asp	Lys	
			150					155					160			
GCC	TAT	GGA	AGT	GGG	ACC	TAC	ATG	GGA	CAA	GCA	AAT	CGA	CTT	GTG	GCC	645
Ala	Tyr	Gly	Ser	Gly	Thr	Tyr	Met	Gly	Gln	Ala	Asn	Arg	Leu	Val	Ala	
		165					170					175				
ATG	AAG	GAG	GTC	GCC	ACT	GGA	AGA	AAC	CCA	AAC	AAG	GAT	CCT	CTA	AAG	693
Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro	Leu	Lys	
	180					185					190					
CTT	GGG	TAC	ACT	TTT	GAG	AGC	ATC	GCG	CAG	CTA	CTT	GAC	ATC	ACA	CTA	741
Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile	Thr	Leu	
195					200					205					210	
CCG	GTA	GGC	CCA	CCC	GGT	GAG	GAT	GAC	AAG	CCC	TGG	GTG	CCA	CTC	ACA	789
Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro	Leu	Thr	
				215					220					225		
AGA	GTG	CCG	TCA	CGG	ATG	TTG	GTG	CTG	ACG	GGA	GAC	GTA	GAT	GGC	GAC	837
Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp	Gly	Asp	
			230					235					240			
TTT	GAG	GTT	GAA	GAT	TAC	CTT	CCC	AAA	ATC	AAC	CTC	AAG	TCA	TCA	AGT	885
Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser	Ser	Ser	
		245					250					255				
GGA	CTA	CCA	TAT	GTA	GGT	CGC	ACC	AAA	GGA	GAG	ACA	ATT	GGC	GAG	ATG	933
Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly	Glu	Met	
	260					265					270					
ATA	GCT	ATC	TCA	AAC	CAG	TTT	CTC	AGA	GAG	CTA	TCA	ACA	CTG	TTG	AAG	981
Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Thr	Leu	Leu	Lys	
275					280					285					290	
CAA	GGT	GCA	GGG	ACA	AAG	GGG	TCA	AAC	AAG	AAG	AAG	CTA	CTC	AGC	ATG	1029
Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu	Ser	Met	
				295					300					305		
TTA	AGT	GAC	TAT	TGG	TAC	TTA	TCA	TGC	GGG	CTT	TTG	TTT	CCA	AAG	GCT	1077
Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro	Lys	Ala	
			310					315					320			
GAA	AGG	TAC	GAC	AAA	AGT	ACA	TGG	CTC	ACC	AAG	ACC	CGG	AAC	ATA	TGG	1125
Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn	Ile	Trp	
		325					330					335				
TCA	GCT	CCA	TCC	CCA	ACA	CAC	CTC	ATG	ATC	TCT	ATG	ATC	ACC	TGG	CCC	1173
Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr	Trp	Pro	
	340					345					350					

GTG Val 355	ATG Met	TCC Ser	AAC Asn	AGC Ser	CCA Pro 360	AAT Asn	AAC Asn	GTG Val	TTG Leu	AAC Asn 365	ATT Ile	GAA Glu	GGG Gly	TGT Cys	CCA Pro 370	1221
TCA Ser	CTC Leu	TAC Tyr	AAA Lys 375	TTC Phe 375	AAC Asn	CCG Pro	TTC Phe	AGA Arg	GGA Gly 380	GGG Gly	TTG Leu	AAC Asn	AGG Arg	ATC Ile 385	GTC Val	1269
GAG Glu	TGG Trp	ATA Ile 390	TTG Leu 390	GCC Ala	CCG Pro	GAA Glu	GAA Glu	CCC Pro 395	AAG Lys	GCT Ala	CTT Leu	GTA Val	TAT Tyr 400	GCG Ala	GAC Asp	1317
AAC Asn	ATA Ile	TAC Tyr 405	ATT Ile	GTC Val	CAC His	TCA Ser	AAC Asn 410	ACG Thr	TGG Trp	TAC Tyr	TCA Ser	ATT Ile 415	GAC Asp	CTA Leu	GAG Glu	1365
AAG Lys	GGT Gly 420	GAG Glu	GCA Ala	AAC Asn	TGC Cys	ACT Thr 425	CGC Arg	CAA Gln	CAC His	ATG Met	CAA Gln 430	GCC Ala	GCA Ala	ATG Met	TAC Tyr	1413
TAC Tyr 435	ATA Ile	CTC Leu	ACC Thr	AGA Arg	GGG Gly 440	TGG Trp	TCA Ser	GAC Asp	AAC Asn	GGC Gly 445	GAC Asp	CCA Pro	ATG Met	TTC Phe	AAT Asn 450	1461
CAA Gln	ACA Thr	TGG Trp	GCC Ala	ACC Thr 455	TTT Phe	GCC Ala	ATG Met	AAC Asn	ATT Ile 460	GCC Ala	CCT Pro	GCT Ala	CTA Leu	GTG Val 465	GTG Val	1509
CAC Asp	TCA Ser	TCG Ser	TGC Cys 470	CTG Leu	ATA Ile	ATG Met	AAC Asn	CTG Leu 475	CAA Gln	ATT Ile	AAG Lys	ACC Thr	TAT Tyr 480	GGT Gly	CAA Gln	1557
GGC Gly	AGC Ser	GGG Gly 485	AAT Asn	GCA Ala	GCC Ala	ACG Thr	TTC Phe 490	ATC Ile	AAC Asn	AAC Asn	CAC His	CTC Leu 495	TTG Leu	AGC Ser	ACA Thr	1605
CTA Leu 500	GTG Val	CTT Leu	GAC Asp	CAG Gln	TGG Trp	AAC Asn 505	CTG Leu	ATG Met	AGA Arg	CAG Gln	CCC Pro 510	AGA Arg	CCA Pro	GAC Asp	AGC Ser	1653
GAG Glu 515	GAG Glu	TTC Phe	AAA Lys	TCA Ser	ATT Ile 520	GAG Glu	GAC Asp	AAG Lys	CTA Leu	GGT Gly 525	ATC Ile	AAC Asn	TTT Phe	AAG Lys	ATT Ile 530	1701
GAG Glu	AGG Arg	TCC Ser	ATT Ile	GAT Asp 535	GAT Asp	ATC Ile	AGG Arg	GGC Gly 540	AAG Lys	CTG Leu	AGA Arg	CAG Gln	CTT Leu	GTC Val 545	CTC Leu	1749
CTT Leu	GCA Ala	CAA Gln	CCA Pro 550	GGG Gly	TAC Tyr	CTG Leu	AGT Ser	GGG Gly 555	GGG Gly	GTT Val	GAA Glu	CCA Pro	GAA Glu	CAA Gln	TCC Ser	1797

AGC Ser	CCA Pro	ACT Thr 565	GTT Val	GAG Glu	CTT Leu	GAC Asp	CTA Leu 570	CTA Leu	GGG Gly	TGG Trp	TCA Ser	GCT Ala 575	ACA Thr	TAC Tyr	AGC Ser	1845
AAA Lys	GAT Asp 580	CTC Leu	GGG Gly	ATC Ile	TAT Tyr	GTG Val 585	CCG Pro	GTG Val	CTT Leu	GAC Asp	AAG Lys 590	GAA Glu	CGC Arg	CTA Leu	TTT Phe	1893
TGT Cys 595	TCT Ser	GCT Ala	GCG Ala	TAT Tyr	CCC Pro 600	AAG Lys	GGA Gly	GTA Val	GAG Glu	AAC Asn 605	AAG Lys	AGT Ser	CTC Leu	AAG Lys	TCC Ser 610	1941
AAA Lys	GTC Val	GGG Gly	ATC Ile	GAG Glu 615	CAG Gln	GCA Ala	TAC Tyr	AAG Lys	GTA Val 620	GTC Val	AGG Arg	TAT Tyr	GAG Glu	GCG Ala 625	TTG Leu	1989
AGG Arg	TTG Leu	GTA Val	GGT Gly 630	GGT Gly	TGG Trp	AAC Asn	TAC Tyr	CCA Pro 635	CTC Leu	CTG Leu	AAC Asn	AAA Lys	GCC Ala 640	TGC Cys	AAG Lys	2037
AAT Asn	AAC Asn	GCA Ala 645	GGC Gly	GCC Ala	GCT Ala	CGG Arg	CGG Arg 650	CAT His	CTG Leu	GAG Glu	GCC Ala	AAG Lys 655	GGG Gly	TTC Phe	CCA Pro	2085
CTC Leu 660	GAC Asp	GAG Glu	TTC Phe	CTA Leu	GCC Ala	GAG Glu 665	TGG Trp	TCT Ser	GAG Glu	CTG Leu	TCA Ser 670	GAG Glu	TTC Phe	GGT Gly	GAG Glu	2133
GCC Ala 675	TTC Phe	GAA Glu	GGC Gly	TTC Phe	AAT Asn 680	ATC Ile	AAG Lys	CTG Leu	ACC Thr	GTA Val 685	ACA Thr	TCT Ser	GAG Glu	AGC Ser	CTA Leu 690	2181
GCC Ala 695	GAA Glu	CTG Leu	AAC Asn	AAG Lys 695	CCA Pro	GTA Val	CCC Pro	CCC Pro	AAG Lys 700	CCC Pro	CCA Pro	AAT Asn	GTC Val 705	AAC Asn	AGA Arg	2229
CCA Pro	GTC Val	AAC Asn	ACT Thr 710	GGG Gly	GGA Gly	CTC Leu	AAG Lys	GCA Ala 715	GTC Val	AGC Ser	AAC Asn	GCC Ala	CTC Leu 720	AAG Lys	ACC Thr	2277
GGT Gly	CGG Arg	TAC Tyr 725	AGG Arg	AAC Asn	GAA Glu	GCC Ala	GGA Gly 730	CTG Leu	AGT Ser	GGT Gly	CTC Leu	GTC Val 735	CTT Leu	CTA Leu	GCC Ala	2325
ACA Thr	GCA Ala 740	AGA Arg	AGC Ser	CGT Arg	CTG Leu	CAA Gln 745	GAT Asp	GCA Ala	GTT Val	AAG Lys	GCC Ala 750	AAG Lys	GCA Ala	GAA Glu	GCC Ala	2373
GAG Glu 755	AAA Lys	CTC Leu	CAC His	AAG Lys	TCC Ser 760	AAG Lys	CCA Pro	GAC Asp	GAC Asp	CCC Pro 765	GAT Asp	GCA Ala	GAC Asp	TGG Trp	TTC Phe 770	2421

GAA AGA TCA GAA ACT CTG TCA GAC CTT CTG GAG AAA GCC GAC ATC GCC	2469
Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp Ile Ala	
775 780 785	
AGC AAG GTC GCC CAC TCA GCA CTC GTG GAA ACA AGC GAC GCC CTT GAA	2517
Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala Leu Glu	
790 795 800	
GCA GTT CAG TCG ACT TCC GTG TAC ACC CCC AAG TAC CCA GAA GTC AAG	2565
Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu Val Lys	
805 810 815	
AAC CCA CAG ACC GCC TCC AAC CCC GTT GTT GGG CTC CAC CTG CCC GCC	2613
Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu Pro Ala	
820 825 830	
AAG AGA GCC ACC GGT GTC CAG GCC GCT CTT CTC GGA GCA GGA ACG AGC	2661
Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly Thr Ser	
835 840 845 850	
AGA CCA ATG GGG ATG GAG GCC CCA ACA CGG TCC AAG AAC GCC GTG AAA	2709
Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala Val Lys	
855 860 865	
ATG GCC AAA CGG CGG CAA CGC CAA AAG GAG AGC CGC TAACAGCCAT	2755
Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg	
870 875	
GATGGGAACC ACTCAAGAAG AGGACACTAA TCCCAGACCC CGTATCCCCG GCCTTCGCCT	2815
CCGGGGGGCCC CC	2827

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 878 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ser	Asp	Ile	Phe	Asn	Ser	Pro	Gln	Ala	Arg	Ser	Thr	Ile	Ser	Ala
1				5					10					15	
Ala	Phe	Gly	Ile	Lys	Pro	Thr	Ala	Gly	Gln	Asp	Val	Glu	Glu	Leu	Leu
			20					25					30		
Ile	Pro	Lys	Val	Trp	Val	Pro	Pro	Glu	Asp	Pro	Leu	Ala	Ser	Pro	Ser
		35					40					45			

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro
 50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
 65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
 85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
 100 105 110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
 115 120 125

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
 130 135 140

Asn Glu Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
 145 150 155 160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Asn Arg Leu
 165 170 175

Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro
 180 185 190

Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile
 195 200 205

Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro
 210 215 220

Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp
 225 230 235 240

Gly Asp Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser
 245 250 255

Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly
 260 265 270

Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Thr Leu
 275 280 285

Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu
 290 295 300

Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro
 305 310 315 320

Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn
 325 330 335
 Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr
 340 345 350
 Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly
 355 360 365
 Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg
 370 375 380
 Ile Val Glu Trp Ile Leu Ala Pro Glu Glu Pro Lys Ala Leu Val Tyr
 385 390 395 400
 Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp
 405 410 415
 Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala
 420 425 430
 Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met
 435 440 445
 Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu
 450 455 460
 Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr
 465 470 475 480
 Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu
 485 490 495
 Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Arg Gln Pro Arg Pro
 500 505 510
 Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe
 515 520 525
 Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu
 530 535 540
 Val Leu Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu
 545 550 555 560
 Gln Ser Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr
 565 570 575
 Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg
 580 585 590

Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu
 595 600 605
 Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
 610 615 620
 Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
 625 630 635 640
 Cys Lys Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly
 645 650 655
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
 660 665 670
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu
 675 680 685
 Ser Leu Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val
 690 695 700
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
 705 710 715 720
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
 725 730 735
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
 740 745 750
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
 770 775 780
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
 820 825 830
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
 835 840 845
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
 850 855 860

Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg
865 870 875

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 97..531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

60	GGATACGATC	GGTCTGACCC	CGGGGGGAGTC	ACCCGGGGGAC	AGGCCGTCAA	GGCCTTG TTC	
114	CAGGATGGGA	CTCCTCCTTC	TACAACGCTA	TCATTG	ATG Met 1	GTT Val	AGT Ser
162	ACA Thr	AAC Asn	GAT Asp	CGC Arg 10	AGC Ser	GAT Asp	GAC Asp
210	TGT Cys	TCC Ser	GTT Val 25	CAT His	ACG Thr	GAG Glu	CCT Pro
258	CAT His	TCC Ser 40	GGA Gly	CGA Arg	CAC His	CCT Pro	GGA Gly 45
306	GAC Asp 55	CTA Leu	CAA Gln	TTT Phe	GAC Asp	TGT Cys 60	GGG Gly
354	TTT Phe	CCC Pro	TGG Trp	ATT Ile	CCC Pro 75	TGG Trp	CTC Leu

GGG CAA TGG GAA CTA CAA GTT CGA TCA GAT GCT CCT GAC TGC CCA GAA	402
Gly Gln Trp Glu Leu Gln Val Arg Ser Asp Ala Pro Asp Cys Pro Glu	
90 95 100	
CCT ACC GGC CAG TTA CAA CTA CTG CAG GCT AGT GAG TCG GAG TCT CAC	450
Pro Thr Gly Gln Leu Gln Leu Gln Ala Ser Glu Ser Glu Ser His	
105 110 115	
AGT GAG GTC AAG CAC ACT TCC TGG TGG CGT TTA TGC ACT AAA CGG CAC	498
Ser Glu Val Lys His Thr Ser Trp Trp Arg Leu Cys Thr Lys Arg His	
120 125 130	
CAT AAA CGC CGT GAC CTT CCA AGG AAG CCT GAG TGA ACTGACA GATGTTAGCT	551
His Lys Arg Arg Asp Leu Pro Arg Lys Pro Glu	
135 140 145	
ACAATGGGTT GATGTCTGCA ACAGCCAACA TCAACGACAA AATTGGGAAC GTCCTAGTAG	611
GGGAAGGGGT CACCGTCCTC AGCTTACCCA CATCATATGA TCTTGGGTAT GTGAGGCTTG	671
GTGACCCCAT TCCCGCAATA GGGCTTGACC CAAAAATGGT AGCCACATGT GACAGCAGTG	731
ACAGGCCCAG AGTCTACACC ATA ACTGCAG CCGATGATTA CCAATTCTCA TCACAGTACC	791
AACCAGGTGG GGTAACAATC ACACTGTTCT CAGCCAACAT TGATGCCATC ACAAGCCTCA	851
GCGTTGGGGG AGAGCTCGTG TTTCAAACAA GCGTCCACGG CCTTGTA CTG GCGGCCACCA	911
CTACCTCAT AGGCTTTGAT GGGACAACGG TAATCACCAG GGCTGTGGCC GCAAACAATG	971
GGCTGACGAC CGGCACCGAC AACCTTATGC CATTCAATCT TGTGATTCCA ACAAACGAGA	1031
TAACCCAGCC AATCACATCC ATCAA ACTGG AGATAGTGAC CTCCAAAAGT GGTGGTCAGG	1091
CAGGGGATCA GATGTCATGG TCGGCAAGAG GGAGCCTAGC AGTGACGATC CATGGTGGCA	1151
ACTATCCAGG GGCCCTCCGT CCCGTCACGC TAGTGGCCTA CGAAAGAGTG GCAACAGGAT	1211
CCGTCGTTAC GGTCGCTGGG GTGAGCAACT TCGAGCTGAT CCCAAATCCT GAACTAGCAA	1271
AGAACCTGGT TACAGAATAC GGCCGATT TG ACCCAGGAGC CATGAACTAC ACAA AATTGA	1331
TACTGAGTGA GAGGGACCGT CTTGGCATCA AGACCGTCTG GCCAACAAGG GAGTACACTG	1391
ACTTTCGTGA ATACTTCATG GAGGTGGCCG ACCTCAACTC TCCCCTGAAG ATTGCAGGAG	1451
CATTGGGCTT CAAAGACATA ATCCGGGCCA TAAGGAGGAT AGCTGTGCCG GTGGTCTCCA	1511
CATTGTTCCC ACCTGCCGCT CCCCTAGCCC ATGCAATTGG GGAAGGTGTA GACTACCTGC	1571
TGGGCGATGA GGCACAGGCT GCTTCAGGAA CTGCTCGAGC CGCGTCAGGA AAAGCAAGAG	1631

CTGCCTCAGG CCGCATAAGG CAGCTGACTC TCGCCGCCGA CAAGGGGTAC GAGGTAGTCG 1691
 CGAATCTATT CCAGGTGCCC CAGAATCCCG TAGTCGACGG GATTCTTGCT TCACCTGGGG 1751
 TACTCCGCGG TGCACACAAC CTCGACTGCG TGTAAAGAGA GGGTGCCACG CTATTCCCTG 1811
 TGGTTATTAC GACAGTGGA A GACGCCATGA CACCCAAAGC ATTGAACAGC AAAATGTTTG 1871
 CTGTCATTGA AGGCGTGCGA GAAGACCTCC AACCTCCATC TCAAAGAGGA TCCTTCATAC 1931
 GAACTCTCTC TGGACACAGA GTCTATGGAT ATGCTCCAGA TGGGGTACTT CCACTGGAGA 1991
 CTGGGAGAGA CTACACCGTT GTCCCAATAG ATGATGTCTG GGACGACAGC ATTATGCTGT 2051
 CCAAAGATCC CATACTCCT ATTGTGGGAA ACAGTGGA A TCTAGCCATA GCTTACATGG 2111
 ATGTGTTTCG ACCCAAAGTC CCAATCCATG TGGCTATGAC GGGAGCCCTC AATGCTTGTG 2171
 GCGAGATTGA GAAAGTAAGC TTTAGAAGCA CCAAGCTCGC CACTGCACAC CGACTTGGCC 2231
 CTAGGTTGGC TGGTCCCGGA GCATTCGATG TAAACACCGG GCCCAACTGG GCAACGTTCA 2291
 TCAAACGTTT CCCTCACAAT CCACGCGACT GGGACAGGCT CCCCTACCTC AACCTACCAT 2351
 ACCTTCCACC CAATGCAGGA CGCCAGTACC ACCTTGCCAT GGCTGCATCA GAGTTCAAAG 2411
 AGACCCCCGA ACTCGAGAGT GCCGTCAGAG CAATGGAAGC AGCAGCCAAC GTGGACCCAC 2471
 TATTCCAATC TGCACTCAGT GTGTTTCATGT GGCTGGAAGA GAATGGGATT GTGACTGACA 2531
 TGGCCAACTT CGCACTCAGC GACCCGAACG CCCATCGGAT GCGAAATTTT CTTGCAAACG 2591
 CACCACAAGC AGGCAGCAAG TCGCAAAGGG CCAAGTACGG GACAGCAGGC TACGGAGTGG 2651
 AGGCTCGGGG CCCACACCA GAGGAAGCAC AGAGGGAAAA AGACACACGG ATCTCAAAGA 2711
 AGATGGAGAC CATGGGCATC TACTTTGCAA CACCAGAATG GGTAGCACTC AATGGGCACC 2771
 GAGGGCCAAG CCCCGGCCAG CTAAAGTACT GGCAGAACAC ACGAGAAATA CCGGACCCAA 2831
 ACGAGGACTA TCTAGACTAC GTGCATGCAG AGAAGAGCCG GTTGGCATCA GAAGAACAAA 2891
 TCCTAAGGGC AGCTACGTCG ATCTACGGGG CTCCAGGACA GGCAGAGCCA CCCCAAGCTT 2951
 TCATAGACGA AGTTGCCAAA GTCTATGAAA TCAACCATGG ACGTGGCCCA AACCAAGAAC 3011
 AGATGAAAGA TCTGCTCTTG ACTGCGATGG AGATGAAGCA TCGCAATCCC AGGCGGGCTC 3071
 TACCAAAGCC CAAGCCAAAA CCCAATGCTC CAACACAGAG ACCCCCTGGT CGGCTGGGCC 3131
 GCTGGATCAG GACCGTCTCT GATGAGGACC TTGAGTGAGG CTCCTGGGAG TCTCCCGACA 3191

CCACCCGCGC AGGTGTGGAC ACCAATTCGG CCTTACAACA TCCCAAATTG GATCCGTTTCG 3251
 CGGGTCCCCT 3261

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala
 1 5 10 15

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
 20 25 30

Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Gly Glu Ala His
 35 40 45

Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
 50 55 60

Val Arg Ala Asn Cys Leu Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly
 65 70 75 80

Cys Ser Leu His Thr Ala Gly Gln Trp Glu Leu Gln Val Arg Ser Asp
 85 90 95

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
 100 105 110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Ser Trp Trp Arg
 115 120 125

Leu Cys Thr Lys Arg His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
 130 135 140

Glu
 145

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION:131..3166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCCGTCAA GGCCTTGTTT 60
 GAGGATGGGA CTCCTCCTTC TACAACGCTA TCATTGATGG TTAGTAGAGA TCAGACAAAC 120
 GATCGCAGCG ATG ACA AAC CTG CAA GAT CAA ACC CAA CAG ATT GTT CCG 169
 Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro
 1 5 10
 TTC ATA CGG AGC CTT CTG ATG CCA ACA ACC GGA CCG GCG TCC ATT CCG 217
 Phe Ile Arg Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro
 15 20 25
 GAC GAC ACC CTG GAG AAG CAC ACT CTC AGG TCA GAG ACC TCG ACC TAC 265
 Asp Asp Thr Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr
 30 35 40 45
 AAT TTG ACT GTG GGG GAC ACA GGG TCA GGG CTA ATT GTC TTT TTC CCT 313
 Asn Leu Thr Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro
 50 55 60
 GGA TTC CCT GGC TCA ATT GTG GGT GCT CAC TAC ACA CTG CAG GGC AAT 361
 Gly Phe Pro Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn
 65 70 75
 GGG AAC TAC AAG TTC GAT CAG ATG CTC CTG ACT GCC CAG AAC CTA CCG 409
 Gly Asn Tyr Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro
 80 85 90
 GCC AGT TAC AAC TAC TGC AGG CTA GTG AGT CGG AGT CTC ACA GTG AGG 457
 Ala Ser Tyr Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg
 95 100 105

TCA Ser 110	AGC Ser	ACA Thr	CTT Leu	CCT Pro	GGT Gly 115	GGC Gly	GTT Val	TAT Tyr	GCA Ala	CTA Leu 120	AAC Asn	GGC Gly	ACC Thr	ATA Ile	AAC Asn 125	505
GCC Ala	GTG Val	ACC Thr	TTC Phe	CAA Gln 130	GGA Gly	AGC Ser	CTG Leu	AGT Ser	GAA Glu 135	CTG Leu	ACA Thr	GAT Asp	GTT Val	AGC Ser 140	TAC Tyr	553
AAT Asn	GGG Gly	TTG Leu	ATG Met 145	TCT Ser	GCA Ala	ACA Thr	GCC Ala	AAC Asn 150	ATC Ile	AAC Asn	GAC Asp	AAA Lys	ATT Ile 155	GGG Gly	AAC Asn	601
GTC Val	CTA Leu	GTA Val 160	GGG Gly	GAA Glu	GGG Gly	GTC Val	ACC Thr 165	GTC Val	CTC Leu	AGC Ser	TTA Leu	CCC Pro 170	ACA Thr	TCA Ser	TAT Tyr	649
GAT Asp 175	CTT Leu	GGG Gly	TAT Tyr	GTG Val	AGG Arg	CTT Leu 180	GGT Gly	GAC Asp	CCC Pro	ATT Ile 185	CCC Pro	GCA Ala	ATA Ile	GGG Gly	CTT Leu	697
GAC Asp 190	CCA Pro	AAA Lys	ATG Met	GTA Val	GCC Ala 195	ACA Thr	TGT Cys	GAC Asp	AGC Ser	AGT Ser 200	GAC Asp	AGG Arg	CCC Pro	AGA Arg	GTC Val 205	745
TAC Tyr	ACC Thr	ATA Ile	ACT Thr	GCA Ala 210	GCC Ala	GAT Asp	GAT Asp	TAC Tyr	CAA Gln 215	TTC Phe	TCA Ser	TCA Ser	CAG Gln 220	TAC Tyr	CAA Gln	793
GCA Pro	GGT Gly	GGG Gly	GTA Val 225	ACA Thr	ATC Ile	ACA Thr	CTG Leu	TTC Phe 230	TCA Ser	GCC Ala	AAC Asn	ATT Ile	GAT Asp 235	GCC Ala	ATC Ile	841
ACA Thr	AGC Ser	CTC Leu 240	AGC Ser	GTT Val	GGG Gly	GGA Gly	GAG Glu 245	CTC Leu	GTG Val	TTT Phe	CAA Gln	ACA Thr 250	AGC Ser	GTC Val	CAC His	889
GGC Gly 255	CTT Leu	GTA Val	CTG Leu	GGC Gly	GCC Ala	ACC Thr 260	ATC Ile	TAC Tyr	CTC Leu	ATA Ile	GGC Gly 265	TTT Phe	GAT Asp	GGG Gly	ACA Thr	937
ACG Thr 270	GTA Val	ATC Ile	ACC Thr	AGG Arg	GCT Ala 275	GTG Val	GCC Ala	GCA Ala	AAC Asn	AAT Asn 280	GGG Gly	CTG Leu	ACG Thr	ACC Thr	GGC Gly 285	985
ACC Thr	GAC Asp	AAC Asn	CTT Leu	ATG Met 290	CCA Pro	TTC Phe	AAT Asn	CTT Leu	GTG Val 295	ATT Ile	CCA Pro	ACA Thr	AAC Asn	GAG Glu 300	ATA Ile	1033
ACC Thr	CAG Gln	CCA Pro	ATC Ile 305	ACA Thr	TCC Ser	ATC Ile	AAA Lys	CTG Leu 310	GAG Glu	ATA Ile	GTG Val	ACC Thr	TCC Ser 315	AAA Lys	AGT Ser	1081

GGT Gly	GGT Gly	CAG Gln 320	GCA Ala	GGG Gly	GAT Asp	CAG Gln 325	ATG Met	TCA Ser	TGG Trp	TCG Ser	GCA Ala	AGA Arg 330	GGG Gly	AGC Ser	CTA Leu	1129
GCA Ala	GTG Val 335	ACG Thr	ATC Ile	CAT His	GGT Gly	GGC Gly 340	AAC Asn	TAT Tyr	CCA Pro	GGG Gly	GCC Ala 345	CTC Leu	CGT Arg	CCC Pro	GTC Val	1177
ACG Thr 350	CTA Leu	GTG Val	GCC Ala	TAC Tyr	GAA Glu 355	AGA Arg	GTG Val	GCA Ala	ACA Thr	GGA Gly 360	TCC Ser	GTC Val	GTT Val	ACG Thr	GTC Val 365	1225
GCT Ala	GGG Gly	GTG Val	AGC Ser	AAC Asn 370	TTC Phe	GAG Glu	CTG Leu	ATC Ile	CCA Pro	AAT Asn	CCT Pro	GAA Glu	CTA Leu	GCA Ala	AAG Lys 380	1273
AAC Asn	CTG Leu	GTT Val	ACA Thr 385	GAA Glu	TAC Tyr	GGC Gly	CGA Arg	TTT Phe 390	GAC Asp	CCA Pro	GGA Gly	GCC Ala	ATG Met 395	AAC Asn	TAC Tyr	1321
ACA Thr	AAA Lys	TTG Leu 400	ATA Ile	CTG Leu	AGT Ser	GAG Glu	AGG Arg 405	GAC Asp	CGT Arg	CTT Leu	GGC Gly	ATC Ile 410	AAG Lys	ACC Thr	GTC Val	1369
TGG Trp 415	CCA Pro	ACA Thr	AGG Arg	GAG Glu	TAC Tyr	ACT Thr 420	GAC Asp	TTT Phe	CGT Arg	GAA Glu	TAC Tyr 425	TTC Phe	ATG Met	GAG Glu	GTG Val	1417
GCC Ala 430	GAC Asp	CTC Leu	AAC Asn	TCT Ser	CCC Pro 435	CTG Leu	AAG Lys	ATT Ile	GCA Ala	GGA Gly 440	GCA Ala	TTC Phe	GGC Gly	TTC Phe	AAA Lys 445	1465
GAC Asp	ATA Ile	ATC Ile	CGG Arg	GCC Ala 450	ATA Ile	AGG Arg	AGG Arg	ATA Ile	GCT Ala 455	GTG Val	CCG Pro	GTG Val	GTC Val	TCC Ser	ACA Thr 460	1513
TTG Leu	TTC Phe	CCA Pro	CCT Pro 465	GCC Ala	GCT Ala	CCC Pro	CTA Leu	GCC Ala 470	CAT His	GCA Ala	ATT Ile	GGG Gly	GAA Glu 475	GGT Gly	GTA Val	1561
GAC Asp	TAC Tyr	CTG Leu 480	CTG Leu	GGC Gly	GAT Asp	GAG Glu	GCA Ala 485	CAG Gln	GCT Ala	GCT Ala	TCA Ser	GGA Gly 490	ACT Thr	GCT Ala	CGA Arg	1609
GCC Ala 495	GCG Ala	TCA Ser	GGA Gly	AAA Lys	GCA Ala	AGA Arg 500	GCT Ala	GCC Ala	TCA Ser	GGC Gly	CGC Arg 505	ATA Ile	AGG Arg	CAG Gln	CTG Leu	1657
ACT Thr 510	CTC Leu	GCC Ala	GCC Ala	GAC Asp	AAG Lys 515	GGG Gly	TAC Tyr	GAG Glu	GTA Val	GTC Val 520	GCG Ala	AAT Asn	CTA Leu	TTC Phe	CAG Gln 525	1705

GTG	CCC	CAG	AAT	CCC	GTA	GTC	GAC	GGG	ATT	CTT	GCT	TCA	CCT	GGG	GTA	1753
Val	Pro	Gln	Asn	Pro	Val	Val	Asp	Gly	Ile	Leu	Ala	Ser	Pro	Gly	Val	
				530					535					540		
CTC	CGC	GGT	GCA	CAC	AAC	CTC	GAC	TGC	GTG	TTA	AGA	GAG	GGT	GCC	ACG	1801
Leu	Arg	Gly	Ala	His	Asn	Leu	Asp	Cys	Val	Leu	Arg	Glu	Gly	Ala	Thr	
			545					550					555			
CTA	TTC	CCT	GTG	GTT	ATT	ACG	ACA	GTG	GAA	GAC	GCC	ATG	ACA	CCC	AAA	1849
Leu	Phe	Pro	Val	Val	Ile	Thr	Thr	Val	Glu	Asp	Ala	Met	Thr	Pro	Lys	
		560					565					570				
GCA	TTG	AAC	AGC	AAA	ATG	TTT	GCT	GTC	ATT	GAA	GGC	GTG	CGA	GAA	GAC	1897
Ala	Leu	Asn	Ser	Lys	Met	Phe	Ala	Val	Ile	Glu	Gly	Val	Arg	Glu	Asp	
	575					580					585					
CTC	CAA	CCT	CCA	TCT	CAA	AGA	GGA	TCC	TTC	ATA	CGA	ACT	CTC	TCT	GGA	1945
Leu	Gln	Pro	Pro	Ser	Gln	Arg	Gly	Ser	Phe	Ile	Arg	Thr	Leu	Ser	Gly	
590					595					600					605	
CAC	AGA	GTC	TAT	GGA	TAT	GCT	CCA	GAT	GGG	GTA	CTT	CCA	CTG	GAG	ACT	1993
His	Arg	Val	Tyr	Gly	Tyr	Ala	Pro	Asp	Gly	Val	Leu	Pro	Leu	Glu	Thr	
				610					615					620		
GGG	AGA	GAC	TAC	ACC	GTT	GTC	CCA	ATA	GAT	GAT	GTC	TGG	GAC	GAC	AGC	2041
Gly	Arg	Asp	Tyr	Thr	Val	Val	Pro	Ile	Asp	Asp	Val	Trp	Asp	Asp	Ser	
			625				630						635			
ATT	ATG	CTG	TCC	AAA	GAT	CCC	ATA	CCT	CCT	ATT	GTG	GGA	AAC	AGT	GGA	2089
Ile	Met	Leu	Ser	Lys	Asp	Pro	Ile	Pro	Pro	Ile	Val	Gly	Asn	Ser	Gly	
		640				645						650				
AAT	CTA	GCC	ATA	GCT	TAC	ATG	GAT	GTG	TTT	CGA	CCC	AAA	GTC	CCA	ATC	2137
Asn	Leu	Ala	Ile	Ala	Tyr	Met	Asp	Val	Phe	Arg	Pro	Lys	Val	Pro	Ile	
	655					660					665					
CAT	GTG	GCT	ATG	ACG	GGA	GCC	CTC	AAT	GCT	TGT	GGC	GAG	ATT	GAG	AAA	2185
His	Val	Ala	Met	Thr	Gly	Ala	Leu	Asn	Ala	Cys	Gly	Glu	Ile	Glu	Lys	
670					675					680					685	
GTA	AGC	TTT	AGA	AGC	ACC	AAG	CTC	GCC	ACT	GCA	CAC	CGA	CTT	GGC	CTT	2233
Val	Ser	Phe	Arg	Ser	Thr	Lys	Leu	Ala	Thr	Ala	His	Arg	Leu	Gly	Leu	
				690					695					700		
AGG	TTG	GCT	GGT	CCC	GGA	GCA	TTC	GAT	GTA	AAC	ACC	GGG	CCC	AAC	TGG	2281
Arg	Leu	Ala	Gly	Pro	Gly	Ala	Phe	Asp	Val	Asn	Thr	Gly	Pro	Asn	Trp	
			705					710					715			
GCA	ACG	TTC	ATC	AAA	CGT	TTC	CCT	CAC	AAT	CCA	CGC	GAC	TGG	GAC	AGG	2329
Ala	Thr	Phe	Ile	Lys	Arg	Phe	Pro	His	Asn	Pro	Arg	Asp	Trp	Asp	Arg	
		720					725					730				

CTC	CCC	TAC	CTC	AAC	CTA	CCA	TAC	CTT	CCA	CCC	AAT	GCA	GGA	CGC	CAG	2377
Leu	Pro	Tyr	Leu	Asn	Leu	Pro	Tyr	Leu	Pro	Pro	Asn	Ala	Gly	Arg	Gln	
	735					740					745					
TAC	CAC	CTT	GCC	ATG	GCT	GCA	TCA	GAG	TTC	AAA	GAG	ACC	CCC	GAA	CTC	2425
Tyr	His	Leu	Ala	Met	Ala	Ala	Ser	Glu	Phe	Lys	Glu	Thr	Pro	Glu	Leu	
750					755					760					765	
GAG	AGT	GCC	GTC	AGA	GCA	ATG	GAA	GCA	GCA	GCC	AAC	GTG	GAC	CCA	CTA	2473
Glu	Ser	Ala	Val	Arg	Ala	Met	Glu	Ala	Ala	Ala	Asn	Val	Asp	Pro	Leu	
				770						775					780	
TTC	CAA	TCT	GCA	CTC	AGT	GTG	TTC	ATG	TGG	CTG	GAA	GAG	AAT	GGG	ATT	2521
Phe	Gln	Ser	Ala	Leu	Ser	Val	Phe	Met	Trp	Leu	Glu	Glu	Asn	Gly	Ile	
			785					790						795		
GTG	ACT	GAC	ATG	GCC	AAC	TTC	GCA	CTC	AGC	GAC	CCG	AAC	GCC	CAT	CGG	2569
Val	Thr	Asp	Met	Ala	Asn	Phe	Ala	Leu	Ser	Asp	Pro	Asn	Ala	His	Arg	
		800					805					810				
ATG	CGA	AAT	TTT	CTT	GCA	AAC	GCA	CCA	CAA	GCA	GGC	AGC	AAG	TCG	CAA	2617
Met	Arg	Asn	Phe	Leu	Ala	Asn	Ala	Pro	Gln	Ala	Gly	Ser	Lys	Ser	Gln	
	815					820					825					
AGG	GCC	AAG	TAC	GGG	ACA	GCA	GGC	TAC	GGA	GTG	GAG	GCT	CGG	GGC	CCC	2665
Arg	Ala	Lys	Tyr	Gly	Thr	Ala	Gly	Tyr	Gly	Val	Glu	Ala	Arg	Gly	Pro	
830					835					840					845	
ACA	CCA	GAG	GAA	GCA	CAG	AGG	GAA	AAA	GAC	ACA	CGG	ATC	TCA	AAG	AAG	2713
Thr	Pro	Glu	Glu	Ala	Gln	Arg	Glu	Lys	Asp	Thr	Arg	Ile	Ser	Lys	Lys	
				850					855						860	
ATG	GAG	ACC	ATG	GGC	ATC	TAC	TTT	GCA	ACA	CCA	GAA	TGG	GTA	GCA	CTC	2761
Met	Glu	Thr	Met	Gly	Ile	Tyr	Phe	Ala	Thr	Pro	Glu	Trp	Val	Ala	Leu	
			865					870					875			
AAT	GGG	CAC	CGA	GGG	CCA	AGC	CCC	GGC	CAG	CTA	AAG	TAC	TGG	CAG	AAC	2809
Asn	Gly	His	Arg	Gly	Pro	Ser	Pro	Gly	Gln	Leu	Lys	Tyr	Trp	Gln	Asn	
		880					885						890			
ACA	CGA	GAA	ATA	CCG	GAC	CCA	AAC	GAG	GAC	TAT	CTA	GAC	TAC	GTG	CAT	2857
Thr	Arg	Glu	Ile	Pro	Asp	Pro	Asn	Glu	Asp	Tyr	Leu	Asp	Tyr	Val	His	
	895					900					905					
GCA	GAG	AAG	AGC	CGG	TTG	GCA	TCA	GAA	GAA	CAA	ATC	CTA	AGG	GCA	GCT	2905
Ala	Glu	Lys	Ser	Arg	Leu	Ala	Ser	Glu	Glu	Gln	Ile	Leu	Arg	Ala	Ala	
910					915					920					925	
ACG	TCG	ATC	TAC	GGG	GCT	CCA	GGA	CAG	GCA	GAG	CCA	CCC	CAA	GCT	TTC	2953
Thr	Ser	Ile	Tyr	Gly	Ala	Pro	Gly	Gln	Ala	Glu	Pro	Pro	Gln	Ala	Phe	
				930					935						940	

ATA GAC GAA GTT GCC AAA GTC TAT GAA ATC AAC CAT GGA CGT GGC CCA 3001
 Ile Asp Glu Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro
 945 950 955

AAC CAA GAA CAG ATG AAA GAT CTG CTC TTG ACT GCG ATG GAG ATG AAG 3049
 Asn Gln Glu Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys
 960 965 970

CAT CGC AAT CCC AGG CGG GCT CTA CCA AAG CCC AAG CCA AAA CCC AAT 3097
 His Arg Asn Pro Arg Arg Ala Leu Pro Lys Pro Lys Pro Lys Pro Asn
 975 980 985

GCT CCA ACA CAG AGA CCC CCT GGT CGG CTG GGC CGC TGG ATC AGG ACC 3145
 Ala Pro Thr Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr
 990 995 1000 1005

GTC TCT GAT GAG GAC CTT GAG TGAGGCTCCT GGGAGTCTCC CGACACCACC 3196
 Val Ser Asp Glu Asp Leu Glu
 1010

CGCGCAGGTG TGGACACCAA TTCGGCCTTA CAACATCCCA AATTGGATCC GTTCGCGGGT 3256

CCCCT 3261

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1012 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
 1 5 10 15
 Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
 20 25 30
 Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
 35 40 45
 Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
 50 55 60
 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn Gly Asn Tyr
 65 70 75 80

Lys	Phe	Asp	Gln	Met	Leu	Leu	Thr	Ala	Gln	Asn	Leu	Pro	Ala	Ser	Tyr	
				85					90					95		
Asn	Tyr	Cys	Arg	Leu	Val	Ser	Arg	Ser	Leu	Thr	Val	Arg	Ser	Ser	Thr	
				100					105					110		
Leu	Pro	Gly	Gly	Val	Tyr	Ala	Leu	Asn	Gly	Thr	Ile	Asn	Ala	Val	Thr	
				115					120					125		
Phe	Gln	Gly	Ser	Leu	Ser	Glu	Leu	Thr	Asp	Val	Ser	Tyr	Asn	Gly	Leu	
				130					135					140		
Met	Ser	Ala	Thr	Ala	Asn	Ile	Asn	Asp	Lys	Ile	Gly	Asn	Val	Leu	Val	
				145					150					155		
Gly	Glu	Gly	Val	Thr	Val	Leu	Ser	Leu	Pro	Thr	Ser	Tyr	Asp	Leu	Gly	
				165					170					175		
Tyr	Val	Arg	Leu	Gly	Asp	Pro	Ile	Pro	Ala	Ile	Gly	Leu	Asp	Pro	Lys	
				180					185					190		
Met	Val	Ala	Thr	Cys	Asp	Ser	Ser	Asp	Arg	Pro	Arg	Val	Tyr	Thr	Ile	
				195					200					205		
Thr	Ala	Ala	Asp	Asp	Tyr	Gln	Phe	Ser	Ser	Gln	Tyr	Gln	Pro	Gly	Gly	
				210					215					220		
Val	Thr	Ile	Thr	Leu	Phe	Ser	Ala	Asn	Ile	Asp	Ala	Ile	Thr	Ser	Leu	
				225					230					235		
Ser	Val	Gly	Gly	Glu	Leu	Val	Phe	Gln	Thr	Ser	Val	His	Gly	Leu	Val	
				245					250					255		
Leu	Gly	Ala	Thr	Ile	Tyr	Leu	Ile	Gly	Phe	Asp	Gly	Thr	Thr	Val	Ile	
				260					265					270		
Thr	Arg	Ala	Val	Ala	Ala	Asn	Asn	Gly	Leu	Thr	Thr	Gly	Thr	Asp	Asn	
				275					280					285		
Leu	Met	Pro	Phe	Asn	Leu	Val	Ile	Pro	Thr	Asn	Glu	Ile	Thr	Gln	Pro	
				290					295					300		
Ile	Thr	Ser	Ile	Lys	Leu	Glu	Ile	Val	Thr	Ser	Lys	Ser	Gly	Gly	Gln	
				305					310					315		
Ala	Gly	Asp	Gln	Met	Ser	Trp	Ser	Ala	Arg	Gly	Ser	Leu	Ala	Val	Thr	
				325					330					335		
Ile	His	Gly	Gly	Asn	Tyr	Pro	Gly	Ala	Leu	Arg	Pro	Val	Thr	Leu	Val	
				340					345					350		

Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val
 355 360 365
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val
 370 375 380
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu
 385 390 395 400
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr
 405 410 415
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu
 420 425 430
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile
 435 440 445
 Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro
 450 455 460
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
 465 470 475 480
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
 485 490 495
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
 500 505 510
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln
 515 520 525
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val Leu Arg Gly
 530 535 540
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro
 545 550 555 560
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn
 565 570 575
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro
 580 585 590
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
 610 615 620

A4

 500
 510
 520
 530
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 560
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 580
 590
 600
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Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu
 625 630 635 640
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala
 645 650 655
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala
 660 665 670
 Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys Val Ser Phe
 675 680 685
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Arg Leu Ala
 690 695 700
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp Ala Thr Phe
 705 710 715 720
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr
 725 730 735
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu
 740 745 750
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala
 755 760 765
 Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser
 770 775 780
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp
 785 790 795 800
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn
 805 810 815
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys
 820 825 830
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu
 835 840 845
 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr
 850 855 860
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His
 865 870 875 880
 Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu
 885 890 895

ACA	AAC	GAT	CGC	AGC	GAT	GAC	AAA	CCT	GCA	AGA	TCA	AAC	CCA	ACA	GAT	162
Thr	Asn	Asp	Arg	Ser	Asp	Asp	Lys	Pro	Ala	Arg	Ser	Asn	Pro	Thr	Asp	
			10					15					20			

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2827 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 112..2745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCATACGATG	GGTCTGACCC	TCTGGGAGTC	ACGAATTAAC	GTGGCTACTA	GGGGCGATAC	60
CCGCCGCTGG	CTGCCACGTT	AGTGGCTCCT	CTTCTTGATG	ATTCTGCCAC	C ATG AGT	117
					Met Ser	
					1	
GAC ATT TTC AAC AGT CCA CAG GCG CGA AGC ACG ATC TCA GCA GCG TTC	165					
Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala Ala Phe						
5 10 15						
GGC ATA AAG CCT ACT GCT GGA CAA GAC GTG GAA GAA CTC TTG ATC CCT	213					
Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu Ile Pro						
20 25 30						
AAA GTT TGG GTG CCA CCT GAG GAT CCG CTT GCC AGC CCT AGT CGA CTG	261					
Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser Arg Leu						
35 40 45 50						
GCA AAG TTC CTC AGA GAG AAC GGC TAC AAA GTT TTG CAG CCG CGG TCT	309					
Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro Arg Ser						
55 60 65						
CTG CCC GAG AAT GAG GAG TAT GAG ACC GAC CAA ATA CTC CCA GAC TTA	357					
Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro Asp Leu						
70 75 80						

GCA	TGG	ATG	CGA	CAG	ATA	GAA	GGG	GCT	GTT	TTA	AAA	CCC	ACT	CTA	TCT	405
Ala	Trp	Met	Arg	Gln	Ile	Glu	Gly	Ala	Val	Leu	Lys	Pro	Thr	Leu	Ser	
	85						90					95				
CTC	CCT	ATT	GGA	GAT	CAG	GAG	TAC	TTC	CCA	AAG	TAC	TAC	CCA	ACA	CAT	453
Leu	Pro	Ile	Gly	Asp	Gln	Glu	Tyr	Phe	Pro	Lys	Tyr	Tyr	Pro	Thr	His	
	100					105					110					
CGC	CCT	AGC	AAG	GAG	AAG	CCC	AAT	GCG	TAC	CCG	CCA	GAC	ATC	GCA	CTA	501
Arg	Pro	Ser	Lys	Glu	Lys	Pro	Asn	Ala	Tyr	Pro	Pro	Asp	Ile	Ala	Leu	
115					120					125					130	
CTC	AAG	CAG	ATG	ATT	TAC	CTG	TTT	CTC	CAG	GTT	CCA	GAG	GCC	AAC	GAG	549
Leu	Lys	Gln	Met	Ile	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Glu	Ala	Asn	Glu	
				135					140					145		
GGC	CTA	AAG	GAT	GAA	GTA	ACC	CTC	TTG	ACC	CAA	AAC	ATA	AGG	GAC	AAG	597
Gly	Leu	Lys	Asp	Glu	Val	Thr	Leu	Leu	Thr	Gln	Asn	Ile	Arg	Asp	Lys	
			150					155					160			
CCC	TAT	GGA	AGT	GGG	ACC	TAC	ATG	GGA	CAA	GCA	ACT	CGA	CTT	GTG	GCC	645
Ala	Tyr	Gly	Ser	Gly	Thr	Tyr	Met	Gly	Gln	Ala	Thr	Arg	Leu	Val	Ala	
		165					170					175				
ATG	AAG	GAG	GTC	GCC	ACT	GGA	AGA	AAC	CCA	AAC	AAG	GAT	CCT	CTA	AAG	693
Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro	Leu	Lys	
	180					185					190					
CTT	GGG	TAC	ACT	TTT	GAG	AGC	ATC	GCG	CAG	CTA	CTT	GAC	ATC	ACA	CTA	741
Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile	Thr	Leu	
195					200					205					210	
CCG	GTA	GGC	CCA	CCC	GGT	GAG	GAT	GAC	AAG	CCC	TGG	GTG	CCA	CTC	ACA	789
Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro	Leu	Thr	
				215					220					225		
AGA	GTG	CCG	TCA	CGG	ATG	TTG	GTG	CTG	ACG	GGA	GAC	GTA	GAT	GGC	GAC	837
Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp	Gly	Asp	
			230					235					240			
TTT	GAG	GTT	GAA	GAT	TAC	CTT	CCC	AAA	ATC	AAC	CTC	AAG	TCA	TCA	AGT	885
Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser	Ser	Ser	
	245						250					255				
GGA	CTA	CCA	TAT	GTA	GGT	CGC	ACC	AAA	GGA	GAG	ACA	ATT	GGC	GAG	ATG	933
Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly	Glu	Met	
	260					265					270					
ATA	GCT	ATA	TCA	AAC	CAG	TTT	CTC	AGA	GAG	CTA	TCA	ACA	CTG	TTG	AAG	981
Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Thr	Leu	Leu	Lys	
275					280					285					290	

CAA	GGT	GCA	GGG	ACA	AAG	GGG	TCA	AAC	AAG	AAG	AAG	CTA	CTC	AGC	ATG	1029
Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu	Ser	Met	
				295					300					305		
TTA	AGT	GAC	TAT	TGG	TAC	TTA	TCA	TGC	GGG	CTT	TTG	TTT	CCA	AAG	GCT	1077
Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro	Lys	Ala	
			310					315					320			
GAA	AGG	TAC	GAC	AAA	AGT	ACA	TGG	CTC	ACC	AAG	ACC	CGG	AAC	ATA	TGG	1125
Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn	Ile	Trp	
		325					330					335				
TCA	GCT	CCA	TCC	CCA	ACA	CAC	CTC	ATG	ATC	TCC	ATG	ATC	ACC	TGG	CCC	1173
Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr	Trp	Pro	
	340					345					350					
GTG	ATG	TCC	AAC	AGC	CCA	AAT	AAC	GTG	TTG	AAC	ATT	GAA	GGG	TGT	CCA	1221
Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly	Cys	Pro	
355					360					365					370	
TCA	CTC	TAC	AAA	TTC	AAC	CCG	TTC	AGA	GGA	GGG	TTG	AAC	AGG	ATC	GTC	1269
Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg	Ile	Val	
				375					380					385		
GAG	TGG	ATA	TTG	GCC	CCG	GAA	GAA	CCC	AAG	GCT	CTT	GTA	TAT	GCG	GAC	1317
Glu	Trp	Ile	Leu	Ala	Pro	Glu	Glu	Pro	Lys	Ala	Leu	Val	Tyr	Ala	Asp	
			390					395					400			
AAC	ATA	TAC	ATT	GTC	CAC	TCA	AAC	ACG	TGG	TAC	TCA	ATT	GAC	CTA	GAG	1365
Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp	Leu	Glu	
		405					410					415				
AAG	GGT	GAG	GCA	AAC	TGC	ACT	CGC	CAA	CAC	ATG	CAA	GCC	GCA	ATG	TAC	1413
Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala	Met	Tyr	
	420					425					430					
TAC	ATA	CTC	ACC	AGA	GGG	TGG	TCA	GAC	AAC	GGC	GAC	CCA	ATG	TTC	AAT	1461
Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met	Phe	Asn	
435					440					445					450	
CAA	ACA	TGG	GCC	ACC	TTT	GCC	ATG	AAC	ATT	GCC	CCT	GCT	CTA	GTG	GTG	1509
Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu	Val	Val	
				455					460					465		
GAC	TCA	TCG	TGC	CTG	ATA	ATG	AAC	CTG	CAA	ATT	AAG	ACC	TAT	GGT	CAA	1557
Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr	Gly	Gln	
			470					475					480			
GGC	AGC	GGG	AAT	GCA	GCC	ACG	TTC	ATC	AAC	AAC	CAC	CTC	TTG	AGC	ACG	1605
Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu	Ser	Thr	
		485					490					495				

CTA	GTG	CTT	GAC	CAG	TGG	AAC	TTG	ATG	AGA	CAG	CCC	AGA	CCA	GAC	AGC	1653
Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Arg	Gln	Pro	Arg	Pro	Asp	Ser	
	500					505					510					
GAG	GAG	TTC	AAA	TCA	ATT	GAG	GAC	AAG	CTA	GGT	ATC	AAC	TTT	AAG	ATT	1701
Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe	Lys	Ile	
515					520					525					530	
GAG	AGG	TCC	ATT	GAT	GAT	ATC	AGG	GGC	AAG	CTG	AGA	CAG	CTT	GTC	CTC	1749
Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu	Val	Leu	
				535					540					545		
CTT	GCA	CAA	CCA	GGG	TAC	CTG	AGT	GGG	GGG	GTT	GAA	CCA	GAA	CAA	TCC	1797
Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu	Gln	Ser	
			550					555					560			
AGC	CCA	ACT	GTT	GAG	CTT	GAC	CTA	CTA	GGG	TGG	TCA	GCT	ACA	TAC	AGC	1845
Ser	Pro	Thr	Val	Glu	Leu	Asp	Leu	Leu	Gly	Trp	Ser	Ala	Thr	Tyr	Ser	
		565					570					575				
AAA	GAT	CTC	GGG	ATC	TAT	GTG	CCG	GTG	CTT	GAC	AAG	GAA	CGC	CTA	TTT	1893
Lys	Asp	Leu	Gly	Ile	Tyr	Val	Pro	Val	Leu	Asp	Lys	Glu	Arg	Leu	Phe	
580						585					590					
TGT	TCT	GCT	GCG	TAT	CCC	AAG	GGA	GTA	GAG	AAC	AAG	AGT	CTC	AAG	TCC	1941
Cys	Ser	Ala	Ala	Tyr	Pro	Lys	Gly	Val	Glu	Asn	Lys	Ser	Leu	Lys	Ser	
595					600					605					610	
AAA	GTC	GGG	ATC	GAG	CAG	GCA	TAC	AAG	GTA	GTC	AGG	TAT	GAG	GCG	TTG	1989
Lys	Val	Gly	Ile	Glu	Gln	Ala	Tyr	Lys	Val	Val	Arg	Tyr	Glu	Ala	Leu	
				615					620					625		
AGG	TTG	GTA	GGT	GGT	TGG	AAC	TAC	CCA	CTC	CTG	AAC	AAA	GCC	TGC	AAG	2037
Arg	Leu	Val	Gly	Gly	Trp	Asn	Tyr	Pro	Leu	Leu	Asn	Lys	Ala	Cys	Lys	
			630				635						640			
AAT	AAC	GCA	GGC	GCC	GCT	CGG	CGG	CAT	CTG	GAG	GCC	AAG	GGG	TTC	CCA	2085
Asn	Asn	Ala	Gly	Ala	Ala	Arg	Arg	His	Leu	Glu	Ala	Lys	Gly	Phe	Pro	
		645					650					655				
CTC	GAC	GAG	TTC	CTA	GCC	GAG	TGG	TCT	GAG	CTG	TCA	GAG	TTC	GGT	GAG	2133
Leu	Asp	Glu	Phe	Leu	Ala	Glu	Trp	Ser	Glu	Leu	Ser	Glu	Phe	Gly	Glu	
	660					665					670					
GCC	TTC	GAA	GGC	TTC	AAT	ATC	AAG	CTG	ACC	GTA	ACA	TCT	GAG	AGC	CTA	2181
Ala	Phe	Glu	Gly	Phe	Asn	Ile	Lys	Leu	Thr	Val	Thr	Ser	Glu	Ser	Leu	
675					680					685					690	
GCC	GAA	CTG	AAC	AAG	CCA	GTA	CCC	CCC	AAG	CCC	CCA	AAT	GTC	AAC	AGA	2229
Ala	Glu	Leu	Asn	Lys	Pro	Val	Pro	Pro	Lys	Pro	Pro	Asn	Val	Asn	Arg	
				695					700					705		

[illegible]